IN THE CLAIMS

Please substitute the claim set in the appendix entitled Clean Version of Pending Claims for the previously pending claim set. The substitute claim set is intended to reflect amendment of previously pending claims 1, 9, 11, 12 and 18. The specific amendments to individual claims are detailed in the following marked up set of claims.

1. (Four Times Amended) A method of determining the presence of a mutation in a target polynucleotide, comprising the steps of:

(a) providing at least two identical polynucleotide probe [micro]arrays, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each array constitute a complete set of n-mers[, wherein each n-mer is at least 8 nucleotides in length];

(b) hybridizing the target polynucleotide to said overhangs of probe polynucleotides in one [micro]array to generate a target hybridization pattern;

(c) hybridizing a reference polynucleotide to said overhangs of probe polynucleotides in a second [micro]array to generate a reference hybridization pattern; and

(d) determining the presence of a mutation in the target polynucleotide by comparing the reference and target hybridization patterns [without sequencing the target polynucleotide]; wherein the method has a false positive rate of less than 1 per 3900 bp.

9. (Once Amended) The method of claim 1, wherein the mutation is an insertion mutation.

11. (Once Amended) The method of claim 1, wherein the [micro]arrays are arranged in parallel.

12. (Four Times Amended) A method of determining whether two or more target polynucleotides are identical [without sequencing the target polynucleotides], comprising the

steps of:

(a) providing at least two identical polynucleotide probe [micro]arrays, wherein each probe comprises a double stranded region and a single-stranded n-mer overhang region such that the overhangs in each [micro]array constitute a complete set of n-mers, wherein each n-mer is at least 8 nucleotides in length;

(b) hybridizing first target polynucleotide to said overhangs of probe polynucleotides in one [micro]array to generate a first hybridization pattern;

(c) hybridizing second target polynucleotide to said overhangs of probe polynucleotides in a second [micro]array to generate a second hybridization pattern; and

(d) comparing the first and second hybridization patterns;

wherein the method has a false positive rate of less than 1 per 3900 bp.

18. (Twice Amended) The method of claim 12, wherein the [micro]arrays are arranged in parallel.

REMARKS

Applicant has carefully reviewed and considered the Office Action mailed on June 13, 2002, and the documents cited therewith. Applicant thanks the Examiner for the telephone interview. Claims 1, 9, 11, 12 and 18 are amended and claims 1-18 are pending in this application.

The claims are directed to hybridization methods for determining the presence of a mutation in a target polynucleotide or for determining whether two or more target polynucleotides are identical without sequencing the target polynucleotides, wherein these methods have a false positive rate of less than 1 per 3900 bp. Applicant submits that the specification discloses that the present methods have a false positive rate of less than 1 per 3900 bp, for example, at Page 7, Lines 8-9; Page 28, Lines 11-12; Page 34, Line 31 to Page 35, Line 3; and Page 36, Lines 27-28. Teminology relating to "without sequencing the target polynucleotide" has been removed from claims 1 and 12. Support for these amendments can be found in originally filed claims 1 and 12, respectfully. The term "microarray" has been amended